

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 18:44:28 : Search time 1502.04 seconds
(without alignments)
786.954 Million cell updates/sec

Title: US-09-486-094-1

Perfect score: 110

Sequence: 1 aggtcgtgtgcagcagat.....gaacgtgtgcagcagtcagg 110

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estfun: *
2: em_esthum: *
3: em_estin: *
4: em_estom: *
5: em_estpl: *
6: em_estba: *
7: em_estro: *
8: em_estov: *
9: em_htc: *
10: gb_estl: *
11: gb_est2: *
12: gb_htc: *
13: gb_gss: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pin: *
18: em_gss_pro: *
19: em_gss_rod: *
20: em_gss_vrt: *
21: em_gss_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.8	28.9	291	10	AA670038
2	31	28.2	169	11	BG051700
3	30	27.3	310	11	BF448402
4	30	27.3	596	13	AZ256542
5	29.8	27.1	517	10	BE584200
6	29.6	26.9	800	13	BH087207
7	29.6	26.9	945	10	AI255552
8	29.4	26.7	376	11	BF704949
9	29.4	26.7	438	11	BG050380
10	29.4	26.7	506	11	BF481432
11	29.4	26.7	561	11	BG559747
12	29.4	26.7	720	11	BI159948

c	13	29.2	26.5	202	11	BI057885
c	14	29.2	26.5	1028	10	BE561966
c	15	29	26.4	718	13	AQ375775
c	16	28.6	26.0	279	10	AA169881
c	17	28.6	26.0	862	11	BF790745
c	18	28.6	26.0	875	11	BG821160
c	19	28.4	25.8	413	10	AA251869
c	20	28.4	25.8	483	10	AI119821
c	21	28.4	25.8	619	10	BE637859
c	22	28.4	25.8	959	11	BG744119
c	23	28.2	25.6	692	10	BE756445
c	24	28.2	25.6	692	10	BE564287
c	25	28.2	25.6	700	13	AZ286787
c	26	28	25.5	433	10	AA860606
c	27	28	25.5	438	10	AA782461
c	28	28	25.5	494	11	NS7477
c	29	28	25.5	740	11	BG175072
c	30	27.8	25.3	303	10	BB554828
c	31	27.8	25.3	359	10	AU065686
c	32	27.8	25.3	437	13	BH126964
c	33	27.8	25.3	555	13	AZ971215
c	34	27.8	25.3	644	10	AW057355
c	35	27.6	25.1	352	10	BE426506
c	36	27.6	25.1	360	10	AW427415
c	37	27.6	25.1	378	11	BF070920
c	38	27.6	25.1	527	10	BE429894
c	39	27.6	25.1	814	11	BG742147
c	40	27.6	25.1	1076	13	CNS058ET
c	41	27.4	24.9	212	10	BB428395
c	42	27.4	24.9	360	11	C70095
c	43	27.4	24.9	378	10	AV203714
c	44	27.4	24.9	449	10	AA104834
c	45	27.4	24.9	459	10	AI391143

ALIGNMENTS

RESULT 1

AA670038

LOCUS 291 bp mRNA

DEFINITION ag39d12.sl Jia bone marrow stroma Homo sapiens cDNA clone

IMAGE:1119191_3, similar to gb:M31682 INHIBIN BETA B CHAIN

PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION AA670038

VERSION AA670038.1

KEYWORDS GI:2631537

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon

, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra

, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Wylie

, T., Waterston, R., Wilson, R. and Francomano, C.

WashU-MGB/NHGRI EST Project

Unpublished (1997)

CONTACT: Wilson RK / Jia L

WashU-MGB/NHGRI EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the

IMaGe Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..291

/organism="Homo sapiens"

FEATURES

source

Qy 1 aggtccgtgtgcaggcagatcaagatctgcaggagggtggttgctactacaagtgc 60

[illegible]


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KEYWORDS
SOURCE      Sorghum propinquum.
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
REFERENCE   1 (bases 1 to 376)
AUTHORS     Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
            ,L.H.

TITLE
JOURNAL     An EST database from Sorghum: floral-induced meristems
COMMENT     Unpublished (2000)
            Contact: Cordonnier-Pratt MM
            Department of Botany
            The University of Georgia
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 542 1805
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: T7
            High quality sequence start: 93
            High quality sequence stop: 334
            POLYA=Yes.

FEATURES
            Location/Qualifiers
            1..376
            /organism="Sorghum propinquum"
            /db_xref="taxon:132711"
            /clone_lib="Floral-Induced Meristem 1 (FM1)"
            /note="Organ: Floral-Induced Meristems; Vector:
            pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
            EcoRI; mature plants were placed in a growth chamber for
            15 days with 16 hr darkness and 8 hr light (flowering is
            induced by short-day conditions); 16 days after being
            returned to the greenhouse under natural long days during
            late April/early May, meristems were harvested the
            library was made from poly-A RNA in the cloning vector
            lambda ZAP II. Clones to be sequenced were prepared by
            mass excision."
BASE COUNT  110 a 83 c 89 g 94 t
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Sequences have been trimmed to exclude polyA, vector and regions below phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: PolyTMix
High quality sequence start: 9
High quality sequence stop: 504
POLYA-No.

```

FEATURES
  source
    1. 506
    /organism="Sorghum propinquum"
    /db_xref="taxon:132711"
    /clone_lib="Floral-Induced Meristem 1 (FM1)"
    /note="Organ: Floral-induced meristems; Vector:
    pluescript II from Lambda zap II; Site_1: XhoI; Site_2:
    EcoRI; mature plants were placed in a growth chamber for
    15 days with 16 hr darkness and 8 hr light (flowering is
    induced by short-day conditions); 16 days after being
    returned to the greenhouse under natural long days during
    late April/early May, meristems were harvested and the
    library was made from poly-A RNA in the cloning vector
    lambda zap II. Clones to be sequenced were prepared by
    mass excision."
  BASE COUNT      129 a 118 c 135 g 124 t
  ORIGIN
    Query Match      26.7%; Score 29.4; DB 11; Length 506;
    Best Local Similarity 60.8%; Pred. No. 1e+02;
    Matches 48; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

  Qy 15 gcagatcaagatctgcaggaggaggtgtgtctactacaagtgcactaacaggccata 74
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Db 204 GGACATGAAGAAGTTTCAGGAAGATGGCATTTTACACAAACAACACTACACGACGCAATA 263
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Qy 75 ctgagctcgcgcgagcgcaa 93
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Db 264 CAGCGGCCCAACACGCGAA 282
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

  RESULT 11
  BG559747
  LOCUS      561 bp mRNA EST 10-APR-2001
  DEFINITION RH122.73_B08.g1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
  sequence.
  ACCESSION BG559747
  VERSION BG559747.1 GI:13588745
  KEYWORDS EST.
  SOURCE      Sorghum propinquum.
  ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
  clade; Panicoideae; Andropogoneae; Sorghum.
  REFERENCE  1 (bases 1 to 561)
  AUTHORS    Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt
  J.L.H.
  TITLE      An EST database from Sorghum: Sorghum propinquum rhizomes
  JOURNAL    Unpublished (2000)
  COMMENT    Contact: Cordonnier-Pratt MM
  Department of Botany
  The University of Georgia
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 542 1805
  Email: mmpratt@uga.edu
  Seq primer: r7
  High quality sequence start: 14
  High quality sequence stop: 561
  POLYA=Yes.
  Location/Qualifiers
    1. .561
    /organism="Sorghum propinquum"
    /db_xref="taxon:132711"
    /clone_lib="Rhizome2 (RH122)"

```

/note="Organ: Rhizomes; Vector: pBluescript II from Lambda zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 144 a 124 c 148 g 145 t
ORIGIN

```

  Query Match      26.7%; Score 29.4; DB 11; Length 561;
  Best Local Similarity 60.8%; Pred. No. 1.1e+02;
  Matches 48; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

  Qy 15 gcagatcaagatctgcaggaggaggtgtgtctactacaagtgcactaacaggccata 74
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Db 223 GGACATGAAGAAGTTTCAGGAAGATGGCATTTTACACAAACAACACTACACGACGCAATA 282
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Qy 75 ctgagctcgcgcgagcgcaa 93
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  Db 283 CAGCGGCCCAACACGCGAA 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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  RESULT 12
  BI159948
  LOCUS      720 bp mRNA EST 05-JUL-2001
  DEFINITION 602863795F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5017943 5',
  mRNA sequence.
  ACCESSION BI159948
  VERSION BI159948.1 GI:14619949
  KEYWORDS EST.
  SOURCE      human.
  ORGANISM    Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE  1 (bases 1 to 720)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-re@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Ling Hong/Rubin Laboratory
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LICM1830 row: n column: 24
  High quality sequence stop: 712.
  Location/Qualifiers
    1. .720
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:5017943"
    /clone_lib="NIH_MGC_42"
    /tissue_type="epithelioid carcinoma cell line"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
    Site_2: EcoRI; cDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGACGAG(G). Size-selected >500bp
    for average insert size 1.8kb. Library constructed by Ling
    Hong in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library. |"

```

FEATURES
source

BASE COUNT
ORIGIN

```

  Query Match      26.7%; Score 29.4; DB 11; Length 720;
  Best Local Similarity 66.7%; Pred. No. 1.1e+02;
  Matches 42; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

LOCUS	AQ375775	718 bp	DNA	GSS	20-MAY-1999
DEFINITION	RPC111-148F23.TJ	RPC11-11	Homo sapiens	genomic clone	RPC11-11.148F23,

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

Map Building

Unpublished (1997)

Other_GSSs: RPCI11-148F23.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

rel: 301 838 0208
Fax: 301 838 0208

Fax: 301 638 0200
Email: hbe@tiq.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (into@resgen.com). BAC end search page: http://www.tlgr.org/tldb/hungen/bac_end_search/bac_end_search.html

http://www.ubgri.
Seq primer: SP6

seq primer: 3PO
Class: BAC ends.

Class: BAC ends: Location:

1. 718 LOCATION

```

I. . / To
/organism="Homo sapiens"

```

```
/organism= Homo sapiens
/db xref="GDB:7556590"
```

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/db_xref=GDB:7336350
/db_xref="taxon:9606"

```

```
/usr_x86_64-linux-gnu/cxx/x86_64-linux-gnu/cxx11abi-148F23"
```

```
/clone lib="RPCI-11"
```

```
/clone_id=
/sex="Male"
```

```
/sex= male
/cell type="Lymphocytes"
```

```

/cell_type= Lymphocytes
/note="Vector: pBACE3.6; site 1: EcoRI; site 2: EcoRI;

```

```
/note= vector: pbac3.0; site=
RPC111 Human Male BAC Library"
```

	NFCIII	human	MAIE	BAC	L1010
205 a	195 c	104 a	214 t		

Query Match 26.4%; Score 29; DB 13; Length 718;
Best Local Similarity 63.8%; Pred. No. 1.4e+02;
Matches 44; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

1 aqgtccgtgttcacagqatcaagatctcagqagqagqggtqggttqctactacaaqtgc 60

305 AASTTCTACAGCAGGCACATCAGCAAAATGGTGAGGAATGGTGGTCTTAGACAGCCT 246

Qy 61 actaacaqq 69

or ac

Search completed: April 2, 2002, 21:04:02
Job time: 8374 sec